

#2



ENTERED

OIPE

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/10/081,408

DATE: 03/11/2002  
 TIME: 10:21:47

Input Set : A:\Ep.txt  
 Output Set: N:\CRF3\03112002\J081408.raw

4 <110> APPLICANT: Abrahms,n , Lars  
 5 Nilsson, Joakim  
 7 <120> TITLE OF INVENTION: METHODS FOR PROTEIN PURIFICATION  
 10 <130> FILE REFERENCE: 13425-053001  
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/081,408  
 C--> 12 <141> CURRENT FILING DATE: 2002-02-21  
 12 <150> PRIOR APPLICATION NUMBER: SE 0100625-3  
 13 <151> PRIOR FILING DATE: 2001-02-23  
 15 <150> PRIOR APPLICATION NUMBER: US 60/272,247  
 16 <151> PRIOR FILING DATE: 2001-02-28  
 18 <160> NUMBER OF SEQ ID NOS: 20  
 20 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
 22 <210> SEQ ID NO: 1  
 23 <211> LENGTH: 4040  
 24 <212> TYPE: DNA  
 25 <213> ORGANISM: Homo sapiens  
 27 <220> FEATURE:  
 28 <221> NAME/KEY: CDS  
 29 <222> LOCATION: (161)...(2449)  
 31 <400> SEQUENCE: 1  
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 33 gccccccacc ccgtccagga gccaacagag ccccgctctt gctggcgatga gaatacattg 120  
 34 ctctcctttg gttgaatcag ctgtccctct tcgtgggaaa atg aac cag aag aca 175  
 35 Met Asn Gln Lys Thr  
 36 1 5  
 38 atc ctc gtg ctc ctc att ctg gcc gtc atc acc atc ttt gcc ttg gtt 223  
 39 Ile Leu Val Leu Leu Ile Leu Ala Val Ile Thr Ile Phe Ala Leu Val  
 40 10 15 20  
 42 tgt gtc ctg ctg gtg ggc agg ggt gga gat ggg ggt gaa ccc agc cag 271  
 43 Cys Val Leu Leu Val Gly Arg Gly Gly Asp Gly Gly Glu Pro Ser Gln  
 44 25 30 35  
 46 ctt ccc cat tgc ccc tct gta tct ccc agt gcc cag cct tgg aca cac 319  
 47 Leu Pro His Cys Pro Ser Val Ser Pro Ser Ala Gln Pro Trp Thr His  
 48 40 45 50  
 50 cct ggc cag agc cag ctg ttt gca gac ctg agc cga gag gag ctg acg 367  
 51 Pro Gly Gln Ser Gln Leu Phe Ala Asp Leu Ser Arg Glu Glu Leu Thr  
 52 55 60 65  
 54 gct gtg atg cgc ttt ctg acc cag cgg ctg ggg cca ggg ctg gtg gat 415  
 55 Ala Val Met Arg Phe Leu Thr Gln Arg Leu Gly Pro Gly Leu Val Asp  
 56 70 75 80 85  
 58 gca gcc cag gcc cgg ccc tcg gac aac tgt gtc ttc tca gtg gag ttg 463  
 59 Ala Ala Gln Ala Arg Pro Ser Asp Asn Cys Val Phe Ser Val Glu Leu  
 60 90 95 100

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62	cag	ctg	cct	ccc	aag	gct	gca	gcc	ctg	gct	cac	ttg	gac	agg	ggg	agc	511
63	Gln	Leu	Pro	Pro	Lys	Ala	Ala	Ala	Leu	Ala	His	Leu	Asp	Arg	Gly	Ser	
64				105					110					115			
66	ccc	cca	cct	gcc	cgg	gag	gca	ctg	gcc	atc	gtc	ttc	ttt	ggc	agg	caa	559
67	Pro	Pro	Pro	Ala	Arg	Glu	Ala	Leu	Ala	Ile	Val	Phe	Phe	Gly	Arg	Gln	
68			120					125					130				
70	ccc	cag	ccc	aac	gtg	agt	gag	ctg	gtg	gtg	ggg	cca	ctg	cct	cac	ccc	607
71	Pro	Gln	Pro	Asn	Val	Ser	Glu	Leu	Val	Val	Gly	Pro	Leu	Pro	His	Pro	
72		135					140				145						
74	tcc	tac	atg	cgg	gac	gtg	act	gtg	gag	cgt	cat	gga	ggc	ccc	ctg	ccc	655
75	Ser	Tyr	Met	Arg	Asp	Val	Thr	Val	Glu	Arg	His	Gly	Gly	Pro	Leu	Pro	
76	150					155				160				165			
78	tat	cac	cga	cgc	ccc	gtg	ctg	ttc	caa	gag	tac	ctg	gac	ata	gac	cag	703
79	Tyr	His	Arg	Arg	Pro	Val	Leu	Phe	Gln	Glu	Tyr	Leu	Asp	Ile	Asp	Gln	
80				170					175					180			
82	atg	atc	ttc	aac	aga	gag	ctg	ccc	cag	gct	tct	ggg	ctt	ctc	cac	cac	751
83	Met	Ile	Phe	Asn	Arg	Glu	Leu	Pro	Gln	Ala	Ser	Gly	Leu	Leu	His	His	
84			185					190					195				
86	tgt	tgc	ttc	tac	aag	cac	cgg	gga	cgg	aac	ctg	gtg	aca	atg	acc	acg	799
87	Cys	Cys	Phe	Tyr	Lys	His	Arg	Gly	Arg	Asn	Leu	Val	Thr	Met	Thr	Thr	
88		200					205				210						
90	gct	ccc	cgt	ggt	ctg	caa	tca	ggg	gac	cgg	gcc	acc	tgg	ttt	ggc	ctc	847
91	Ala	Pro	Arg	Gly	Leu	Gln	Ser	Gly	Asp	Arg	Ala	Thr	Trp	Phe	Gly	Leu	
92		215				220				225							
94	tac	tac	aac	atc	tgc	ggc	gct	ggg	ttc	ttc	ctg	cac	cac	gtg	ggc	ttg	895
95	Tyr	Tyr	Asn	Ile	Ser	Gly	Ala	Gly	Phe	Phe	Leu	His	His	Val	Gly	Leu	
96	230			235				240			245						
98	gag	ctg	cta	gtg	aac	cac	aag	gcc	ctt	gac	cct	gcc	cgc	tgg	act	atc	943
99	Glu	Leu	Leu	Val	Asn	His	Lys	Ala	Leu	Asp	Pro	Ala	Arg	Trp	Thr	Ile	
100			250					255			260						
102	cag	aag	gtg	ttc	tat	caa	ggc	cgc	tac	tac	gac	agc	ctg	gcc	cag	ctg	991
103	Gln	Lys	Val	Phe	Tyr	Gln	Gly	Arg	Tyr	Tyr	Asp	Ser	Leu	Ala	Gln	Leu	
104			265					270			275						
106	gag	gcc	cag	ttt	gag	gcc	ggc	ctg	gtg	aat	gtg	gtg	ctg	atc	cca	gac	1039
107	Glu	Ala	Gln	Phe	Glu	Ala	Gly	Leu	Val	Asn	Val	Val	Leu	Ile	Pro	Asp	
108		280					285				290						
110	aat	ggc	aca	ggt	ggg	tcc	tgg	tcc	ctg	aag	tcc	cct	gtg	ccc	ccg	ggt	1087
111	Asn	Gly	Thr	Gly	Gly	Ser	Trp	Ser	Leu	Lys	Ser	Pro	Val	Pro	Pro	Gly	
112		295				300					305						
114	cca	gct	ccc	cct	cta	cag	ttc	tat	ccc	caa	ggc	ccc	cgc	ttc	agt	gtc	1135
115	Pro	Ala	Pro	Pro	Leu	Gln	Phe	Tyr	Pro	Gln	Gly	Pro	Arg	Phe	Ser	Val	
116	310				315				320				325				
118	cag	gga	agt	cga	gtg	gcc	tcc	tca	ctg	tgg	act	ttc	tcc	ttt	ggc	ctc	1183
119	Gln	Gly	Ser	Arg	Val	Ala	Ser	Ser	Leu	Trp	Thr	Phe	Ser	Phe	Gly	Leu	
120			330					335			340						
122	gga	gca	ttc	agt	ggc	cca	agg	atc	ttt	gac	ggt	cgc	ttc	caa	gga	gaa	1231
123	Gly	Ala	Phe	Ser	Gly	Pro	Arg	Ile	Phe	Asp	Val	Arg	Phe	Gln	Gly	Glu	
124			345					350			355						
126	aga	cta	ggt	tat	gag	ata	agc	ctc	caa	gag	gcc	ttg	gcc	atc	tat	ggt	1279

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127 Arg Leu Val Tyr Glu Ile Ser Leu Gln Glu Ala Leu Ala Ile Tyr Gly
128          360          365          370
130 gga aat tcc cca gca gca atg acg acc cgc tat gtg gat gga ggc ttt      1327
131 Gly Asn Ser Pro Ala Ala Met Thr Thr Arg Tyr Val Asp Gly Gly Phe
132          375          380          385
134 ggc atg ggc aag tac acc acg ccc ctg acc cgt ggg gtg gac tgc ccc      1375
135 Gly Met Gly Lys Tyr Thr Thr Pro Leu Thr Arg Gly Val Asp Cys Pro
136 390          395          400          405
138 tac ttg gcc acc tac gtg gac tgg cac ttc ctt ttg gag tcc cag gcc      1423
139 Tyr Leu Ala Thr Tyr Val Asp Trp His Phe Leu Leu Glu Ser Gln Ala
140          410          415          420
142 ccc aag aca ata cgt gat gcc ttt tgt gtg ttt gaa cag aac cag ggc      1471
143 Pro Lys Thr Ile Arg Asp Ala Phe Cys Val Phe Glu Gln Asn Gln Gly
144          425          430          435
146 ctc ccc ctg cgg cga cac cac tca gat ctc tac tcg cac tac ttt ggg      1519
147 Leu Pro Leu Arg Arg His His Ser Asp Leu Tyr Ser His Tyr Phe Gly
148          440          445          450
150 ggt ctt gcg gaa acg gtg ctg gtc gtc aga tct atg tcc acc ttg ctc      1567
151 Gly Leu Ala Glu Thr Val Leu Val Val Arg Ser Met Ser Thr Leu Leu
152          455          460          465
154 aac tat gac tat gtg tgg gat acg gtc ttc cac ccc agt ggg gcc ata      1615
155 Asn Tyr Asp Tyr Val Trp Asp Thr Val Phe His Pro Ser Gly Ala Ile
156 470          475          480          485
158 gaa ata cga ttc tat gcc acg ggc tac atc agc tcg gca ttc ctc ttt      1663
159 Glu Ile Arg Phe Tyr Ala Thr Gly Tyr Ile Ser Ser Ala Phe Leu Phe
160          490          495          500
162 ggt gct act ggg aag tac ggg aac caa gtg tca gag cac acc ctg ggc      1711
163 Gly Ala Thr Gly Lys Tyr Gly Asn Gln Val Ser Glu His Thr Leu Gly
164          505          510          515
166 acg gtc cac acc cac agc gcc cac ttc aag gtg gat ctg gat gta gca      1759
167 Thr Val His Thr His Ser Ala His Phe Lys Val Asp Leu Asp Val Ala
168          520          525          530
170 gga ctg gag aac tgg gtc tgg gcc gag gat atg gtc ttt gtc ccc atg      1807
171 Gly Leu Glu Asn Trp Val Trp Ala Glu Asp Met Val Phe Val Pro Met
172          535          540          545
174 gct gtg ccc tgg agc cct gag cac cag ctg cag agg ctg cag gtg acc      1855
175 Ala Val Pro Trp Ser Pro Glu His Gln Leu Gln Arg Leu Gln Val Thr
176 550          555          560          565
178 cgg aag ctg ctg gag atg gag gag cag gcc gcc ttc ctc gtg gga agc      1903
179 Arg Lys Leu Leu Glu Met Glu Glu Gln Ala Ala Phe Leu Val Gly Ser
180          570          575          580
182 gcc acc cct cgc tac ctg tac ctg gcc agc aac cac agc aac aag tgg      1951
183 Ala Thr Pro Arg Tyr Leu Tyr Leu Ala Ser Asn His Ser Asn Lys Trp
184          585          590          595
186 ggt cac ccc cgg ggc tac cgc atc cag atg ctc agc ttt gct gga gag      1999
187 Gly His Pro Arg Gly Tyr Arg Ile Gln Met Leu Ser Phe Ala Gly Glu
188          600          605          610
190 ccg ctg ccc caa aac agc tcc atg gcg aga ggc ttc agc tgg gag agg      2047
191 Pro Leu Pro Gln Asn Ser Ser Met Ala Arg Gly Phe Ser Trp Glu Arg

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192	615	620	625	
194	tac cag ctg gct gtg acc cag cgg aag gag gag gag ccc agt agc agc	2095		
195	Tyr Gln Leu Ala Val Thr Gln Arg Lys Glu Glu Glu Pro Ser Ser Ser			
196	630 635 640 645			
198	agc gtt ttc aat cag aat gac cct tgg gcc ccc act gtg gat ttc agt	2143		
199	Ser Val Phe Asn Gln Asn Asp Pro Trp Ala Pro Thr Val Asp Phe Ser			
200	650 655 660			
202	gac ttc atc aac aat gag acc att gct gga aag gat ttg gtg gcc tgg	2191		
203	Asp Phe Ile Asn Asn Glu Thr Ile Ala Gly Lys Asp Leu Val Ala Trp			
204	665 670 675			
206	gtg aca gct ggt ttt ctg cat atc cca cat gca gag gac att cct aac	2239		
207	Val Thr Ala Gly Phe Leu His Ile Pro His Ala Glu Asp Ile Pro Asn			
208	680 685 690			
210	aca gtg act gtg ggg aac ggc gtg ggc ttc ttc ctc cga ccc tat aac	2287		
211	Thr Val Thr Val Gly Asn Gly Val Gly Phe Phe Leu Arg Pro Tyr Asn			
212	695 700 705			
214	ttc ttt gac gaa gac ccc tcc ttc tac tct gcc gac tcc atc tac ttc	2335		
215	Phe Phe Asp Glu Asp Pro Ser Phe Tyr Ser Ala Asp Ser Ile Tyr Phe			
216	710 715 720 725			
218	cga ggg gac cag gat gct ggg gcc tgc gag gtc aac ccc cta gct tgc	2383		
219	Arg Gly Asp Gln Asp Ala Gly Ala Cys Glu Val Asn Pro Leu Ala Cys			
220	730 735 740			
222	ctg ccc cag gct gct gcc tgt gcc ccc gac ctc cct gcc ttc tcc cac	2431		
223	Leu Pro Gln Ala Ala Ala Cys Ala Pro Asp Leu Pro Ala Phe Ser His			
224	745 750 755			
226	ggg ggc ttc tct cac aac taggcggtcc tgggatgggg catgtggcca	2479		
227	Gly Gly Phe Ser His Asn			
228	760			
230	agggctccag ggccagggtg tgagggatgg ggagcagctg ggcaactgggc cggcagcctg	2539		
231	gttccctctt tccgtgcca ggactctctt tcttccacta cccctccctcg catccgcctc	2599		
232	tgagccagga gcctcctgac cctgtgatgc ctgacacagg ggacactgaa ccttgttgat	2659		
233	gccagctgta ctgagttctc atccacagag gccaggcatg gccagcctg gaggcgtggc	2719		
234	cgagggtctc cctagatggt tccctttgtt gctgtctggc tttcccgaat ctttttaggc	2779		
235	cacctccaag gactctaaaa gggggctatt ccctggagac cccagagtag ggttgccagt	2839		
236	cctgcaagtc catagctgag ctggaaagga tgcttctgct cacattccct ctcatccagg	2899		
237	tcctttcctt ctogtcttcc tctctctcac ctacttccct ctcctccctcc tgttcctgcc	2959		
238	ttctcttcta tccgtcaatt tctcccgaat cctgagggga tatccctatg tcccagcccc	3019		
239	tggtactccc ccagccctca gttttcagtc aagtctcgtc tcctctccag ccctatggaa	3079		
240	gtctcaaggt caagggaacc ctaatcagag tggccaatcc ctgtgtgtcg ttcccttggtg	3139		
241	tctgttgctt attgggagta ggagttgctc ctaccctgtt cctggggctg ggtgtgtttc	3199		
242	aggacagctg cttctgtgca tttgtgtctg cctgcctcat gctctctata gaggaggatg	3259		
243	gtcatcgtga cagcagcagc tcaagttagc atttcaagtg atttgggggt gcaatgataa	3319		
244	tgaagaatgg ccattttgta ccagggtctt gtattctgca acagcctgtt tgggaggctg	3379		
245	gagtggaaac aaagggtggg catcaaagat gagaagccaa agcccctaca actccagcca	3439		
246	cccagccagg aggggtgtc caatcacatt caggcatgcg aatgagctgg gccctgggtg	3499		
247	aggtgggggt ctggcctagt ggggaggggc ctggcctggg tggggcaggg cctggcctgg	3559		
248	tccaggcttg ggtccattc ccactactgc tgcctcctct gaggtctgga ttggggatgg	3619		
249	ggacaaagaa atagcaagag atgagaaaca acagaaactt ttttctctaa aggactggtt	3679		
250	aatcaattc tgatacagcc ttacaatata atagtatgca gctaaaaaat aattgtatgt	3739		

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```

251 ctttatatac taatatgtaa taatcttcag gtgaaaaagg caagccacag aaatgtgtat 3799
252 agcgcacttc ccatttgtgt ttcagaaaagg agtagaatat aaacacataa ttgcttatgt 3859
253 atgcctattc agaataaatg' ggtaaacactg attacttttg ggaggggaac cagtaggttg 3919
254 aggacaggag agggaagggt cttaaacactt acaccctttt gtacattttg aattttgaac 3979
255 catgtgactg tattacctat tcaaaaataaa caataaatgg gcccaaaaaa aaaaaaaaaa 4039
256 a 4040
258 <210> SEQ ID NO: 2
259 <211> LENGTH: 763
260 <212> TYPE: PRT
261 <213> ORGANISM: Homo sapiens
263 <400> SEQUENCE: 2
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267 20 25 30
268 Gly Glu Pro Ser Gln Leu Pro His Cys Pro Ser Val Ser Pro Ser Ala
269 35 40 45
270 Gln Pro Trp Thr His Pro Gly Gln Ser Gln Leu Phe Ala Asp Leu Ser
271 50 55 60
272 Arg Glu Glu Leu Thr Ala Val Met Arg Phe Leu Thr Gln Arg Leu Gly
273 65 70 75 80
274 Pro Gly Leu Val Asp Ala Ala Gln Ala Arg Pro Ser Asp Asn Cys Val
275 85 90 95
276 Phe Ser Val Glu Leu Gln Leu Pro Pro Lys Ala Ala Ala Leu Ala His
277 100 105 110
278 Leu Asp Arg Gly Ser Pro Pro Pro Ala Arg Glu Ala Leu Ala Ile Val
279 115 120 125
280 Phe Phe Gly Arg Gln Pro Gln Pro Asn Val Ser Glu Leu Val Val Gly
281 130 135 140
282 Pro Leu Pro His Pro Ser Tyr Met Arg Asp Val Thr Val Glu Arg His
283 145 150 155 160
284 Gly Gly Pro Leu Pro Tyr His Arg Arg Pro Val Leu Phe Gln Glu Tyr
285 165 170 175
286 Leu Asp Ile Asp Gln Met Ile Phe Asn Arg Glu Leu Pro Gln Ala Ser
287 180 185 190
288 Gly Leu Leu His His Cys Cys Phe Tyr Lys His Arg Gly Arg Asn Leu
289 195 200 205
290 Val Thr Met Thr Thr Ala Pro Arg Gly Leu Gln Ser Gly Asp Arg Ala
291 210 215 220
292 Thr Trp Phe Gly Leu Tyr Tyr Asn Ile Ser Gly Ala Gly Phe Phe Leu
293 225 230 235 240
294 His His Val Gly Leu Glu Leu Leu Val Asn His Lys Ala Leu Asp Pro
295 245 250 255
296 Ala Arg Trp Thr Ile Gln Lys Val Phe Tyr Gln Gly Arg Tyr Tyr Asp
297 260 265 270
298 Ser Leu Ala Gln Leu Glu Ala Gln Phe Glu Ala Gly Leu Val Asn Val
299 275 280 285
300 Val Leu Ile Pro Asp Asn Gly Thr Gly Gly Ser Trp Ser Leu Lys Ser
301 290 295 300

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Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY

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PATENT APPLICATION: US/10/081,408

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Input Set : A:\Ep.txt

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L:12 M:270 C: Current Application Number differs, Replaced Current Application No

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date